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CTG AGA TAC ACA CCT CAT CCA GCA TAT GCT ACC TTT TGC AGG CCA AAG GAG AAC TGG TGG 189

Q Y T Q G R R Y A S T P Q K F Y L T P P 83
CAG TAC ACC CAA GGA AGG AGA TAT GCT TCC ACA CCA CAG AAA TTT TAC CTC ACA CCT CCA 249

Q V N S I L K A N E Y S F K V P E F D G 103
CAA GTC AAT AGC ATC CTT AAA GCT AAT GAA TAC AGT TTC AAA GTG CCA GAA TTT GAC GGC 309

K N V S S I L G F D S N Q L P A N A P I 123
AAA AAT GTC AGT TCT ATC CTT GGA TTT GAC AGC AAT CAG CTG CCT GCA AAT GCA CCC ATT 369

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GAG GAC CGG AGA AGT GCA GCA ACC TGC TTG CAG ACC AGA GGG ATG CTT TTG GGG GTT TTT 429

D G H A G C A C S Q A V S E R L F Y Y I 163
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A V S L L P H E T L L E I E N A V E S G 183
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T G E S T D I D V K E A L I N A F K R L 243
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095070 2927050

Fig. 1A

09801237.070801
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2/6

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CGG	CTG	AAA	TTG	GAA	CAT	CCA	AAG	AGT	GAG	GCC	AAG	AGT	GTC	GTG	AAA	CAG	GAT	CGG	CTG	1029
L	G	L	L	M	P	F	R	A	F	G	D	V	K	F	K	W	S	I	D	363
CIT	GGC	TTG	CTG	ATG	CCA	TTT	AGG	GCA	TTT	GGA	GAT	GTA	AAG	TTC	AAA	TGG	AGC	ATT	GAC	1089
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CIT	CAA	AAG	AGA	GTG	ATA	GAA	TCT	GGC	CCA	GAC	CAG	TTG	AAT	GAC	AAT	GAA	TAT	ACC	AAG	1149
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L	S	L	P	E	E	L	A	R	M	Y	R	D	D	I	T	I	I	V	V	523
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Q	F	N	S	H	V	V	G	A	Y	Q	N	Q	F	*						538
CAG	TTC	AAT	TCT	CAT	GTT	GTA	GGG	GCG	TAT	CAA	AAC	CAA	GAA	TAG						1614

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Fig. 1B

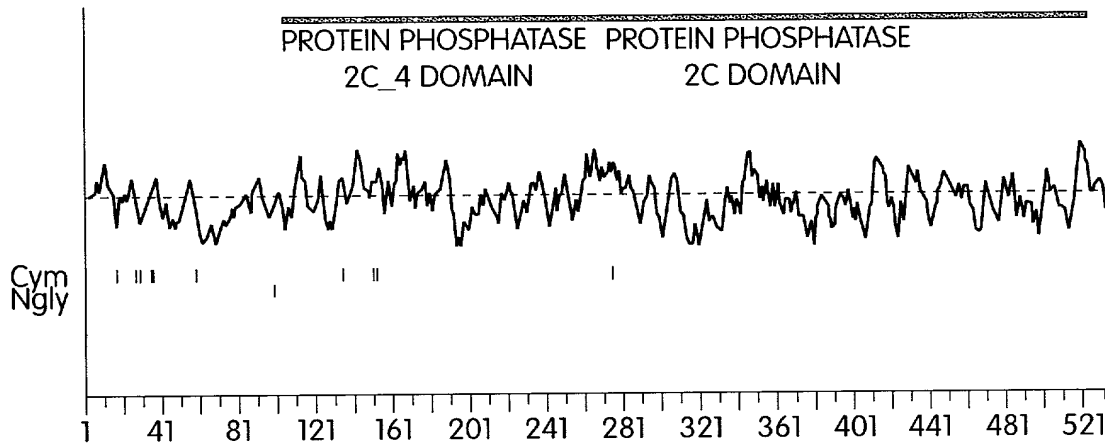


Fig. 2

PP2C: domain 1 of 1, from 173 to 461: score 261.3, E = 1.3e-74

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 1 ++++ + r +++ +++++ ++ s++ s+ +f +++ +
 26583 173 LLEIENAVESGRALLPILQWHKHPNDYF-SKEASKLYFNLSLRTYWQE 218 SEQ ID NO:2
 qaakyagkhlhk.tilaerksfpegdpwEmklsdledalkesfleadtd
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 26583 219 LIDLNTGESTDIdVKEALINAFKRLDN-----DISLEAQVGDPSNFLNY 262
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 26583 350 FRAFGDVFKWSIDLQKRVIeSgPdQLNDnEYTKFiPPnyhtpPYLTAEP 399
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 +vt +++l+p+ D+F1+LA+DGLW++++ q+vv iv + l+ + +
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 meaaeklvdeaiargaeDni<-*
 ++ ++ + + g ++
 26583 442 HQQPIAVGGYKVTLGQMHGL 461

Fig. 3A

PP2C_4: domain 1 of 1, from 99 to 523: score 338.5, E = 7.6e-98

```

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26583  245 NDIIsleaqvdpnsflnylvlrvaafsgATACVAHVDGVDLHVANTGDSRA 294

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26583  295 MLGVQEEdgSW-----SAVTLSNDHNAQNERELERLKEHPKSE--AKS 336

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      +++++ ++l r+ +++++   +++L +++   +++ + +D+iT++v
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      v
26583  523 V      523

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Fig. 3B

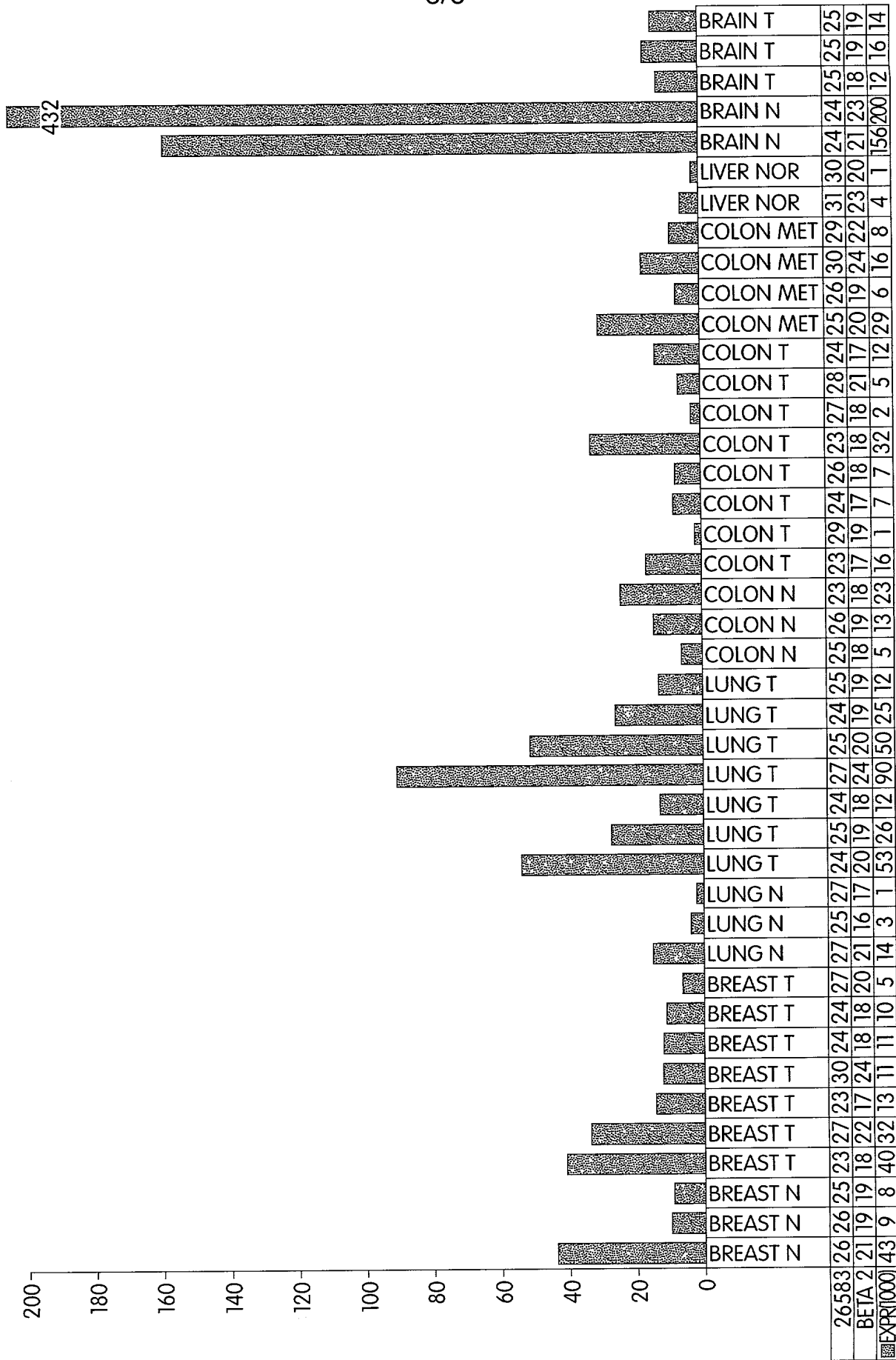


Fig. 4